What is claimed is:

1.   A polypeptide chain useful as a subunit of a
dimeric osteogenic protein comprising a pair of
disulfide-bonded polypeptide chains,
        said polypeptide chain having an amino acid
sequence sufficiently duplicative of Sequence ID No.
1 or Sequence ID No. 3 such that the dimeric
osteogenic protein comprising said polypeptide chain
has a conformation capable of inducing endochondral
bone formation when implanted in a mammal in
association with a matrix.

2.   The polypeptide chain of claim 1 wherein the
sequence comprises (Sequence ID No. 1):

<div align="center">mOP-2</div>

Ala 1	Ala	Arg	Pro	Leu 5	Lys	Arg	Arg	Gln
Pro 10	Lys	Lys	Thr	Asn	Glu 15	Leu	Pro	His
Pro	Asn 20	Lys	Leu	Pro	Gly	Ile 25	Phe	Asp
Asp	Gly	His 30	Gly	Ser	Arg	Gly	Arg 35	Glu
Val	Cys	Arg	Arg 40	His	Glu	Leu	Tyr	Val 45
Arg	Phe	Arg	Asp	Leu 50	Gly	Trp	Leu	Asp
Trp 55	Val	Ile	Ala	Pro	Gln 60	Gly	Tyr	Ser

Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90
Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
				95				
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100					105			
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
	110					115		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
		120					125	
Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
			130					135
Cys	Gly	Cys	His.					

3.   The polypeptide chain of claim 1 wherein the sequence comprises (Sequence ID No. 3):

hOP-2

Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
10					15			
Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
	20					25		
Asp	Val	Asn	Gly	Ser	His	Gly	Arg	Gln
		30					35	
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40					45

```
Ser   Phe   Gln   Asp   Leu   Gly   Trp   Leu   Asp
                        50

Trp   Val   Ile   Ala   Pro   Gln   Gly   Tyr   Ser
55                            60

Ala   Tyr   Tyr   Cys   Glu   Gly   Glu   Cys   Ser
      65                            70

Phe   Pro   Leu   Asp   Ser   Cys   Met   Asn   Ala
            75                            80

Thr   Asn   His   Ala   Ile   Leu   Gln   Ser   Leu
                  85                            90

Val   His   Leu   Met   Lys   Pro   Asn   Ala   Val
                        95

Pro   Lys   Ala   Cys   Cys   Ala   Pro   Thr   Lys
100                           105

Leu   Ser   Ala   Thr   Ser   Val   Leu   Tyr   Tyr
      110                           115

Asp   Ser   Ser   Asn   Asn   Val   Ile   Leu   Arg
            120                           125

Lys   Ala   Arg   Asn   Met   Val   Val   Lys   Ala
                  130                           135

Cys   Gly   Cys   His.
```

4.   The polypeptide chain of claim 1 wherein the
sequence comprises (Sequence ID No. 7):

```
Cys   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa
 1                      5                            10

Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa
                  15                            20

Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Cys   Xaa   Xaa   Xaa
                  25                            30

Cys   Xaa   Xaa   Xaa   Xaa   Xaa   Cys   Xaa   Xaa   Xaa   Xaa
            35                            40
```

```
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
45              50                      55

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
               60                      65

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
           70                  75

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
       80                  85

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
   90                  95

Xaa Cys Xaa
100
```

and wherein each Xaa independently represents one of the 20 naturally occurring L-isomer, α-amino acids, and together with said 8 cysteine residues define said polypeptide chain.

5.   The polypeptide chain of claim 1 wherein the sequence comprises (Sequence ID No. 8):

```
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5                      10

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
               15                  20

Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
       25                  30

Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
       35                  40

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
45              50                      55

Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa
               60                      65
```

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                    70   75

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            80   85

Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa
        90   95

wherein each Xaa independently represents one of the 20 naturally occurring L-isomer, α-amino acids, and together with said 7 cysteine residues define said polypeptide chain.

6.   A polypeptide chain useful as a subunit of a dimeric osteogenic protein, said protein being capable of inducing endochondral bone formation when implanted in a mammal in association with a matrix;
        said polypeptide chain comprising the amino acid sequence (Sequence ID No. 5):

Cys Xaa_1 Xaa_2 His Glu Leu Tyr Val Xaa_3 Phe
 1   5   10

Xaa_4 Asp Leu Gly Trp Xaa_5 Asp Trp Xaa_6 Ile
                    15   20

Ala Pro Xaa_7 Gly Tyr Xaa_8 Ala Tyr Tyr Cys
                25   30

Glu Gly Cys Xaa_9 Phe Pro Leu Xaa_{10} Ser Xaa_{11}
                35   40

Met Asn Ala Thr Asn His Ala Ile Xaa_{12} Thr
                45   50

Leu Xaa_{13} Xaa_{14} Xaa_{15} Xaa_{16} Xaa_{17} Xaa_{18} Val
                    55

Pro Lys Xaa_{19} Cys Cys Ala Pro Thr Xaa_{20} Leu
        60   65

Xaa_{21} Ala Xaa_{22} Ser Val Leu Tyr Xaa_{23} Asp
                    70   75

Xaa_{24} Ser Xaa_{25} Asn Val Xaa_{26} Leu Xaa_{27} Lys
                    80   85

Xaa_{28} Pro Asn Met Val Val Xaa_{29} Ala Cys Gly
                    90   95

Cys His,

wherein Xaa_1 = (Lys or Arg); Xaa_2 = (Lys or Arg); Xaa_3 = (Ser or Arg); Xaa_4 = (Arg or Gln); Xaa_5 = (Gln or Leu); Xaa_6 = (Ile or Val); Xaa_7 = (Glu or Gln); Xaa_8 = (Ala or Ser); Xaa_9 = (Ala or Ser); Xaa_{10} = (Asn or Asp); Xaa_{11} = (Tyr or Cys); Xaa_{12} = (Val or Leu); Xaa_{13} = (His or Asn); Xaa_{14} = (Phe or Leu); Xaa_{15} = (Ile or Met); Xaa_{16} = (Asn or Lys); Xaa_{17} = (Glu, Asp or Asn); Xaa_{18} = (Thr, Ala or Val); Xaa_{19} = (Pro or Ala); Xaa_{20} = (Gln or Lys); Xaa_{21} = (Asn or Ser); Xaa_{22} = (Ile or Thr); Xaa_{23} = (Phe or Tyr); Xaa_{24} = (Asp, Glu or Ser); Xaa_{25} = (Ser or Asn); Xaa_{26} = (Ile or Asp); Xaa_{27} = (Lys or Arg); Xaa_{28} = (Tyr, Ala or His); and Xaa_{29} = (Arg or Lys).

7.   The polypeptide chain of claim 6 wherein Xaa_{11} = Cys.

8.   A polypeptide chain useful as a subunit of a dimeric osteogenic protein, said protein being capable of inducing endochondral bone formation when implanted in a mammal in association with a matrix;
        the amino acid sequence of said polypeptide chain being at least 70% homologous with the amino acid sequence (Sequence ID No. 1):

mOP-2

Ala 1	Ala	Arg	Pro	Leu 5	Lys	Arg	Arg	Gln
Pro 10	Lys	Lys	Thr	Asn	Glu 15	Leu	Pro	His
Pro	Asn 20	Lys	Leu	Pro	Gly	Ile 25	Phe	Asp
Asp	Gly	His 30	Gly	Ser	Arg	Gly	Arg 35	Glu
Val	Cys	Arg	Arg 40	His	Glu	Leu	Tyr	Val 45
Arg	Phe	Arg	Asp	Leu 50	Gly	Trp	Leu	Asp
Trp 55	Val	Ile	Ala	Pro	Gln 60	Gly	Tyr	Ser
Ala	Tyr 65	Tyr	Cys	Glu	Gly	Glu 70	Cys	Ala
Phe	Pro	Leu 75	Asp	Ser	Cys	Met	Asn 80	Ala
Thr	Asn	His	Ala 85	Ile	Leu	Gln	Ser	Leu 90
Val	His	Leu	Met	Lys 95	Pro	Asp	Val	Val
Pro 100	Lys	Ala	Cys	Cys	Ala 105	Pro	Thr	Lys
Leu	Ser 110	Ala	Thr	Ser	Val	Leu 115	Tyr	Tyr
Asp	Ser	Ser 120	Asn	Asn	Val	Ile	Leu 125	Arg
Lys	His	Arg	Asn 130	Met	Val	Val	Lys	Ala 135
Cys	Gly	Cys	His.				

9.   The polypeptide chain of claim 8 wherein the amino acid sequence is at least 80% homologous with the amino acid sequence (Sequence ID No. 1):

mOP-2

Ala 1	Ala	Arg	Pro	Leu 5	Lys	Arg	Arg	Gln
Pro 10	Lys	Lys	Thr	Asn	Glu 15	Leu	Pro	His
Pro	Asn 20	Lys	Leu	Pro	Gly	Ile 25	Phe	Asp
Asp	Gly	His 30	Gly	Ser	Arg	Gly	Arg 35	Glu
Val	Cys	Arg	Arg 40	His	Glu	Leu	Tyr	Val 45
Arg	Phe	Arg	Asp	Leu 50	Gly	Trp	Leu	Asp
Trp 55	Val	Ile	Ala	Pro	Gln 60	Gly	Tyr	Ser
Ala	Tyr 65	Tyr	Cys	Glu	Gly	Glu 70	Cys	Ala
Phe	Pro	Leu 75	Asp	Ser	Cys	Met	Asn 80	Ala
Thr	Asn	His	Ala 85	Ile	Leu	Gln	Ser	Leu 90
Val	His	Leu	Met	Lys 95	Pro	Asp	Val	Val
Pro 100	Lys	Ala	Cys	Cys	Ala 105	Pro	Thr	Lys
Leu	Ser 110	Ala	Thr	Ser	Val	Leu 115	Tyr	Tyr
Asp	Ser	Ser 120	Asn	Asn	Val	Ile	Leu 125	Arg

Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
			130					135

Cys Gly Cys His.

10.   The polypeptide chain of claim 8 wherein the amino acid sequence comprises (Sequence ID No. 1):

<u>mOP-2</u>

Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln
1				5				

Pro	Lys	Lys	Thr	Asn	Glu	Leu	Pro	His
10					15			

Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp
	20					25		

Asp	Gly	His	Gly	Ser	Arg	Gly	Arg	Glu
		30					35	

Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40					45

Arg	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp
				50				

Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
55					60			

Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		

Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	

Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90

Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
				95				

Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100					105			

Leu   Ser   Ala   Thr   Ser   Val   Leu   Tyr   Tyr
      110   115

Asp   Ser   Ser   Asn   Asn   Val   Ile   Leu   Arg
            120   125

Lys   His   Arg   Asn   Met   Val   Val   Lys   Ala
                  130   135

Cys   Gly   Cys   His.

11.   The polypeptide chain of claim 8 wherein the
amino acid sequence comprises (Sequence ID No. 3):

hOP-2

Ala   Val   Arg   Pro   Leu   Arg   Arg   Arg   Gln
 1   5

Pro   Lys   Lys   Ser   Asn   Glu   Leu   Pro   Gln
10   15

Ala   Asn   Arg   Leu   Pro   Gly   Ile   Phe   Asp
      20   25

Asp   Val   Asn   Gly   Ser   His   Gly   Arg   Gln
            30   35

Val   Cys   Arg   Arg   His   Glu   Leu   Tyr   Val
                  40   45

Ser   Phe   Gln   Asp   Leu   Gly   Trp   Leu   Asp
                        50

Trp   Val   Ile   Ala   Pro   Gln   Gly   Tyr   Ser
55   60

Ala   Tyr   Tyr   Cys   Glu   Gly   Glu   Cys   Ser
      65   70

Phe   Pro   Leu   Asp   Ser   Cys   Met   Asn   Ala
            75   80

Thr   Asn   His   Ala   Ile   Leu   Gln   Ser   Leu
                  85   90

```
Val    His    Leu    Met    Lys    Pro    Asn    Ala    Val
                            95

Pro    Lys    Ala    Cys    Cys    Ala    Pro    Thr    Lys
100                                105

Leu    Ser    Ala    Thr    Ser    Val    Leu    Tyr    Tyr
       110                                115

Asp    Glu    Ser    Asn    Asn    Val    Ile    Leu    Arg
              120                                125

Lys    Ala    Arg    Asn    Met    Val    Val    Lys    Ala
                     130                                135

Cys    Gly    Cys    His.
```

12.   The polypeptide chain of claim 8 wherein the amino acid sequence comprises (SEQ ID NO. 9):

<u>hOP-2P</u>

```
                     Pro    Leu    Arg    Arg    Arg    Gln
                      1                           5

Pro    Lys    Lys    Ser    Asn    Glu    Leu    Pro    Gln
                     10                                 15

Ala    Asn    Arg    Leu    Pro    Gly    Ile    Phe    Asp
                            20

Asp    Val    Asn    Gly    Ser    His    Gly    Arg    Gln
25                                 30

Val    Cys    Arg    Arg    His    Glu    Leu    Tyr    Val
       35                                 40

Ser    Phe    Gln    Asp    Leu    Gly    Trp    Leu    Asp
              45                                 50

Tyr    Val    Ile    Ala    Pro    Gln    Gly    Tyr    Ser
                     55                                 60

Ala    Tyr    Tyr    Cys    Glu    Gly    Glu    Cys    Ser
                            65
```

Phe 70	Pro	Leu	Asp	Ser	Cys 75	Met	Asn	Ala
Thr	Asn 80	His	Ala	Ile	Leu	Gln 85	Ser	Leu
Val	His	Leu 90	Met	Lys	Pro	Asn	Ala 95	Val
Pro	Lys	Ala	Cys 100	Cys	Ala	Pro	Thr	Lys 105
Leu	Ser	Ala	Thr	Ser 110	Val	Leu	Tyr	Tyr
Asp 115	Glu	Ser	Asn	Asn	Val 120	Ile	Leu	Arg
Lys	Ala 125	Arg	Asn	Met	Val	Val 130	Lys	Ala
Cys	Gly	Cys 135	His.					

13.   The polypeptide chain of claim 8 wherein the amino acid sequence comprises (SEQ ID NO. 10):

<u>hOP-2R</u>

						Arg 1	Arg	Gln
Pro	Lys 5	Lys	Ser	Asn	Glu	Leu 10	Pro	Gln
Ala	Asn	Arg 15	Leu	Pro	Gly	Ile	Phe 20	Asp
Asp	Val	Asn	Gly 25	Ser	His	Gly	Arg	Gln 30
Val	Cys	Arg	Arg	His 35	Glu	Leu	Tyr	Val

Ser 40	Phe	Gln	Asp	Leu	Gly 45	Trp	Leu	Asp
Tyr	Val 50	Ile	Ala	Pro	Gln	Gly 55	Tyr	Ser
Ala	Tyr	Tyr 60	Cys	Glu	Gly	Glu	Cys 65	Ser
Phe	Pro	Leu	Asp 70	Ser	Cys	Met	Asn	Ala 75
Thr	Asn	His	Ala	Ile 80	Leu	Gln	Ser	Leu
Val 85	His	Leu	Met	Lys	Pro 90	Asn	Ala	Val
Pro	Lys 95	Ala	Cys	Cys	Ala	Pro 100	Thr	Lys
Leu	Ser	Ala 105	Thr	Ser	Val	Leu	Tyr 110	Tyr
Asp	Glu	Ser	Asn 115	Asn	Val	Ile	Leu	Arg 120
Lys	Ala	Arg	Asn	Met 125	Val	Val	Lys	Ala
Cys 130	Gly	Cys	His.					

14.   The polypeptide chain of claim 8 wherein the amino acid sequence comprises (SEQ ID NO. 11):

<u>hOP-2S</u>

						Ser 1	Gln	Gln
Pro	Phe 5	Val	Val	Thr	Phe	Phe 10	Arg	Ala
Ser	Pro	Ser 15	Pro	Ile	Arg	Thr	Pro 20	Arg

Ala	Val	Arg	Pro 25	Leu	Arg	Arg	Arg	Gln 30
Pro	Lys	Lys	Ser	Asn 35	Glu	Leu	Pro	Gln
Ala 40	Asn	Arg	Leu	Pro	Gly 45	Ile	Phe	Asp
Asp	Val 50	Asn	Gly	Ser	His	Gly 55	Arg	Gln
Val	Cys	Arg 60	Arg	His	Glu	Leu	Tyr 65	Val
Ser	Phe	Gln	Asp 70	Leu	Gly	Trp	Leu	Asp 75
Tyr	Val	Ile	Ala	Pro 80	Gln	Gly	Tyr	Ser
Ala 85	Tyr	Tyr	Cys	Glu	Gly 90	Glu	Cys	Ser
Phe	Pro 95	Leu	Asp	Ser	Cys	Met 100	Asn	Ala
Thr	Asn	His 105	Ala	Ile	Leu	Gln	Ser 110	Leu
Val	His	Leu	Met 115	Lys	Pro	Asn	Ala	Val 120
Pro	Lys	Ala	Cys	Cys 125	Ala	Pro	Thr	Lys
Leu 130	Ser	Ala	Thr	Ser	Val 135	Leu	Tyr	Tyr
Asp	Glu 140	Ser	Asn	Asn	Val	Ile 145	Leu	Arg
Lys	Ala	Arg 150	Asn	Met	Val	Val	Lys 165	Ala
Cys	Gly	Cys	His. 170					

15.   A polypeptide chain useful as a subunit of a
dimeric osteogenic protein, said protein being
capable of inducing endochondral bone formation when
implanted in a mammal in association with a matrix;
said polypeptide chain having an amino acid
sequence comprising (Sequence ID No. 2):

Prepro mOP-2

	Met	Ala	Met	Arg	Pro	Gly	Pro	Leu
	1				5			
Trp	Leu	Leu	Gly	Leu	Ala	Leu	Cys	Ala
	10					15		
Leu	Gly	Gly	Gly	His	Gly	Pro	Gly	Pro
		20					25	
Pro	His	Thr	Cys	Pro	Gln	Arg	Arg	Leu
			30					35
Gly	Ala	Arg	Asp	Arg	Asp	Met	Gln	Arg
				40				
Glu	Ile	Leu	Ala	Val	Leu	Gly	Leu	Pro
45					50			
Gly	Arg	Pro	Asp	Pro	Val	His	Asn	Pro
	55					60		
Pro	Leu	Pro	Gly	Thr	Gln	Arg	Ala	Pro
		65				70		
Leu	Phe	Met	Leu	Asp	Leu	Tyr	His	Ala
			70				80	
Met	Thr	Asp	Asp	Asp	Asp	Gly	Gly	Pro
				85				
Pro	Gln	Ala	His	Leu	Gly	Arg	Ala	Asp
90					95			
Leu	Val	Met	Ser	Phe	Val	Asn	Met	Val
	100					105		

Glu	Arg	Asp 110	Arg	Thr	Leu	Gly	Tyr 115	Gln
Glu	Pro	His	Trp 120	Lys	Glu	Phe	His	Phe 125
Asp	Leu	Thr	Gln	Ile 130	Pro	Ala	Gly	Glu
Ala 135	Val	Thr	Ala	Ala	Glu 140	Phe	Arg	Ile
Tyr	Lys 145	Glu	Pro	Ser	Thr	His 150	Pro	Leu
Asn	Thr	Thr 155	Leu	His	Ile	Ser	Met 160	Phe
Glu	Val	Val	Gln 165	Glu	His	Ser	Asn	Arg 170
Glu	Ser	Asp	Leu	Phe 175	Phe	Leu	Asp	Leu
Gln 180	Thr	Leu	Arg	Ser	Gly 185	Asp	Glu	Gly
Trp	Leu 190	Val	Leu	Asp	Ile	Thr 195	Ala	Ala
Ser	Asp	Arg 200	Trp	Leu	Leu	Asn	His 205	His
Lys	Asp	Leu	Gly 210	Leu	Arg	Leu	Tyr	Val 215
Glu	Thr	Ala	Asp	Gly 220	His	Ser	Met	Asp
Pro 225	Gly	Leu	Ala	Gly	Leu 230	Leu	Gly	Arg
Gln	Ala 235	Pro	Arg	Ser	Arg	Gln 240	Pro	Phe
Met	Val	Thr 245	Phe	Phe	Arg	Ala	Ser 250	Gln
Ser	Pro	Val	Arg 255	Ala	Pro	Arg	Ala	Ala 260

Arg	Pro	Leu	Lys	Arg 265	Arg	Gln	Pro	Lys
Lys 270	Thr	Asn	Glu	Leu	Pro 275	His	Pro	Asn
Lys	Leu 280	Pro	Gly	Ile	Phe	Asp 285	Asp	Gly
His	Gly	Ser 290	Arg	Gly	Arg	Glu	Val 295	Cys
Arg	Arg	His	Glu 300	Leu	Tyr	Val	Arg	Phe 305
Arg	Asp	Leu	Gly	Trp 310	Leu	Asp	Trp	Val
Ile 315	Ala	Pro	Gln	Gly	Tyr 320	Ser	Ala	Tyr
Tyr	Cys 325	Glu	Gly	Glu	Cys	Ala 330	Phe	Pro
Leu	Asp	Ser 335	Cys	Met	Asn	Ala	Thr 340	Asn
His	Ala	Ile	Leu 345	Gln	Ser	Leu	Val	His 350
Leu	Met	Lys	Pro	Asp 355	Val	Val	Pro	Lys
Ala 360	Cys	Cys	Ala	Pro	Thr 365	Lys	Leu	Ser
Ala	Thr 370	Ser	Val	Leu	Tyr	Tyr 375	Asp	Ser
Ser	Asn	Asn 380	Val	Ile	Leu	Arg	Lys 385	His
Arg	Asn	Met	Val 390	Val	Lys	Ala	Cys	Gly 395
Cys	His.							

16.   A polypeptide chain useful as a subunit of a
dimeric osteogenic protein, said protein being

capable of inducing endochondral bone formation when implanted in a mammal in association with a matrix;

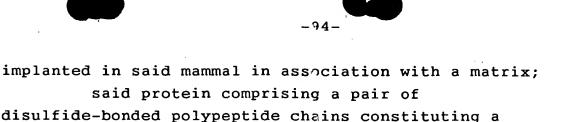said polypeptide chain comprising the amino acid sequence (Sequence ID No. 4):

Prepro hOP-2

Met	Thr	Ala	Leu	Pro	Gly	Pro	Leu	Trp
1				5				
Leu	Leu	Gly	Leu	Ala	Leu	Cys	Ala	Leu
10				15				
Gly	Gly	Gly	Gly	Pro	Gly	Leu	Arg	Pro
	20				25			
Pro	Pro	Gly	Cys	Pro	Gln	Arg	Arg	Leu
		30					35	
Gly	Ala	Arg	Asp	Arg	Asp	Val	Gln	Arg
			40					45
Glu	Ile	Leu	Ala	Val	Leu	Gly	Leu	Pro
				50				
Gly	Arg	Pro	Arg	Pro	Arg	Ala	Pro	Pro
55					60			
Ala	Ala	Ser	Arg	Leu	Pro	Ala	Ser	Ala
	65					70		
Pro	Leu	Phe	Met	Leu	Asp	Leu	Tyr	His
		75					80	
Arg	Met	Ala	Gly	Asp	Asp	Asp	Glu	Asp
			85					90
Gly	Ala	Ala	Glu	Ala	Leu	Gly	Arg	Ala
				95				
Asp	Leu	Val	Met	Ser	Phe	Val	Asn	Met
100					105			
Val	Glu	Arg	Asp	Arg	Ala	Leu	Gly	His
	110					115		

Gln Glu Pro His Trp Lys Glu Phe Arg
          120   125

Phe Asp Leu Thr Gln Ile Pro Ala Gly
          130   135

Glu Ala Val Thr Ala Ala Glu Phe Arg
                    140

Ile Tyr Lys Val Pro Ser Ile His Leu
145   150

Leu Asn Arg Thr Leu His Val Ser Met
     155   160

Phe Gln Val Val Gln Glu Gln Ser Asn
          165   170

Arg Glu Ser Asp Leu Phe Phe Leu Asp
               175   180

Leu Gln Thr Leu Arg Ala Gly Asp Glu
                    185

Gly Trp Leu Val Leu Asp Val Thr Ala
190   195

Ala Ser Asp Cys Trp Leu Leu Lys Arg
     200   205

His Lys Asp Leu Gly Leu Arg Leu Tyr
          210   215

Val Glu Thr Glu Asp Gly His Ser Val
               220   225

Asp Pro Gly Leu Ala Gly Leu Leu Gly
                    230

Gln Arg Ala Pro Arg Ser Gln Gln Pro
235   240

Phe Val Val Thr Phe Phe Arg Ala Ser
     245   250

Pro Ser Pro Ile Arg Thr Pro Arg Ala
          255   260

Val	Arg	Pro	Leu 265	Arg	Arg	Arg	Gln	Pro 270
Lys	Lys	Ser	Asn	Glu 275	Leu	Pro	Gln	Ala
Asn 280	Arg	Leu	Pro	Gly	Ile 285	Phe	Asp	Asp
Val	His 290	Gly	Ser	His	Gly	Arg 295	Gln	Val
Cys	Arg	Arg 300	His	Glu	Leu	Tyr	Val 305	Ser
Phe	Gln	Asp	Leu 310	Gly	Trp	Leu	Asp	Trp 315
Val	Ile	Ala	Pro	Gln 320	Gly	Tyr	Ser	Ala
Tyr 325	Tyr	Cys	Glu	Gly	Glu 330	Cys	Ser	Phe
Pro	Leu 335	Asp	Ser	Cys	Met	Asn 340	Ala	Thr
Asn	His 345	Ala	Ile	Leu	Gln	Ser	Leu 350	Val
His	Leu	Met	Lys 355	Pro	Asn	Ala	Val	Pro 360
Lys	Ala	Cys	Cys	Ala 365	Pro	Thr	Lys	Leu
Ser 370	Ala	Thr	Ser	Val	Leu 375	Tyr	Tyr	Asp
Ser	Ser 380	Asn	Asn	Val	Ile	Leu 385	Arg	Lys
Ala	Arg	Asn 390	Met	Val	Val	Lys	Ala 395	Cys
Gly	Cys	His.						

17.   A dimeric osteogenic protein capable of inducing endochondral bone formation in a mammal when

implanted in said mammal in association with a matrix;

said protein comprising a pair of disulfide-bonded polypeptide chains constituting a dimeric species, wherein each said polypeptide chain is the polypeptide chain of claim 1, 6, 8, 15 or 16.

18.   The polypeptide chain of claim 1, 6, 8, 15 or 16 produced by expression of recombinant DNA in a host cell.

19.   The polypeptide chain of claim 15 wherein said host cell is a procaryotic host cell.

20.   The polypeptide chain of claim 15 wherein said host cell is a mammalian cell.

21.   The polypeptide of claim 1, 6, 8, 15 or 16 that is glycosylated.

22.   A DNA encoding the polypeptide chain of claim 1, 6, 8, 15 or 16.

23.   A dimeric protein comprising a pair of polypeptide chains expressed from a DNA sequence sufficiently duplicative of the sequence of Sequence ID No. 2 or Sequence ID No. 4 such that, when said polypeptide chains are oxidized to produce a disulfide-bonded dimeric species, the dimeric species has a conformation that is capable of inducing endochondral bone or cartilage formation when disposed within a matrix and implanted in a mammal.